

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT:

- (A) NAME: Kanton Zuerich vertreten durch die
Erziehungsdirektion
(B) STREET: Walchetur
(C) CITY: Zuerich
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(E) COUNTRY: Switzerland
(F) POSTAL CODE (ZIP): CH-8090
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(ii) TITLE OF INVENTION: Immunological Detection of Prions

(iii) NUMBER OF SEQUENCES: 9

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(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: EP 97102837.8
(B) FILING DATE: 21-FEB-1997

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bos taurus
(D) DEVELOPMENTAL STAGE: Adult

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(vii) IMMEDIATE SOURCE:

- (B) CLONE: pbPrP3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAAGAAGC GACCAAAACC TGGAGGAGGA TGGAACACTG GGGGGAGCCG ATACCCAGGA 60
CAGGGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAGGGAG GGGGTGGCTG GGGTCAGCCC 120

CATGGAGGTG GCTGGGGCCA GCCTCATGGA GGTGGCTGGG GCCAGCCTCA TGGAGGTGGC 180
 TGGGGTCAGC CCCATGGTGG TGGCTGGGGA CAGCCACATG GTGGTGGAGG CTGGGGTCAA 240
 5 GGTGGTACCC ACGGTCAATG GAACAAACCC AGTAAGCCAA AAACCAACAT GAAGCATGTG 300
 GCAGGAGCTG CTGCAGCTGG AGCAGTGGTA GGGGGCCTTG GTGGCTACAT GCTGGGAAGT 360
 GCCATGAGCA GGCCTCTTAT ACATTTTGGC AGTGACTATG AGGACCGTTA CTATCGTGAA 420
 10 AACATGCACC GTTACCCCAA CCAAGTGTAC TACAGGCCAG TGGATCAGTA TAGTAACCAG 480
 AACAACTTTG TGCATGACTG TGTCAACATC ACAGTCAAGG AACACACAGT CACCACCACC 540
 15 ACCAAGGGGG AGAACTTCAC CGAAACTGAC ATCAAGATGA TGGAGCGAGT GGTGGAGCAA 600
 ATGTGCATTA CCCAGTACCA GAGAGAATCC CAGGCTTATT ACCAACGAGG GGCAAGTTAA 660

20 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: Bos taurus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

40 Met Lys Lys Arg Pro Lys Pro Gly Gly Gly Trp Asn Thr Gly Gly Ser
 1 5 10 15
 Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
 20 25 30
 45 Gly Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
 35 40 45
 His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
 50 55 60
 His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Gly Trp Gly Gln
 65 70 75 80
 55 Gly Gly Thr His Gly Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn
 85 90 95
 Met Lys His Val Ala Gly Ala Ala Ala Ala Gly Ala Val Val Gly Gly
 100 105 110

Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro Leu Ile His
 115 120 125
 5 Phe Gly Ser Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn Met His Arg
 130 135 140
 Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Gln Tyr Ser Asn Gln
 145 150 155 160
 10 Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Val Lys Glu His Thr
 165 170 175
 Val Thr Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu Thr Asp Ile Lys
 15 180 185 190
 Met Met Glu Arg Val Val Glu Gln Met Cys Ile Thr Gln Tyr Gln Arg
 195 200 205
 20 Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Ala Ser
 210 215

(2) INFORMATION FOR SEQ ID NO: 3:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"
 (iii) HYPOTHETICAL: NO
 35 (iv) ANTI-SENSE: NO
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGAATTCCA TATGAAGAAG CGACCAAAAC CTG

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45 (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"
 55 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGGGATCCTA TTAAGTTGCC CCTCGTTGGT A

31

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Leu Ile His Phe Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

10 Gly Ser Asp Tyr Glu Asp Arg
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(2) INFORMATION FOR SEQ ID NO: 8:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

25 (iv) ANTI-SENSE: NO

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Tyr Tyr Arg Pro Val Asp Gln Tyr Ser
1 5

35 (2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

45 (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55 Cys Ile Thr Gln Tyr Gln Arg Glu Ser Gln Ala Tyr Tyr
1 5 10